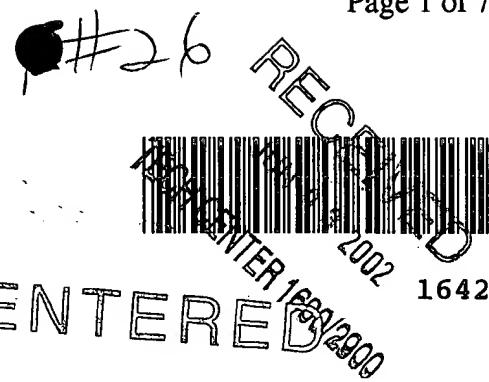


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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/202,047A

DATE: 05/07/2002

TIME: 15:57:05

Input Set : A:\2002-04-22 0020-4491P seq list.txt
 Output Set: N:\CRF3\05072002\I202047A.raw

3 <110> APPLICANT: ITOH, Kyogo
 4 SHICHIJO, Shigeki
 5 IMAI, Yasuhisa
 7 <120> TITLE OF INVENTION: TUMOR ANTIGEN PROTEINS, GENES THEREFOR, AND TUMOR
 8 ANTIGEN PEPTIDES
 10 <130> FILE REFERENCE: 0020-4491P
 12 <140> CURRENT APPLICATION NUMBER: 09/202,047A
 13 <141> CURRENT FILING DATE: 1998-12-07
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2527
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_feature
 26 <222> LOCATION: (1)..(2527)
 27 <223> OTHER INFORMATION: Strandedness: Double-stranded
 29 <220> FEATURE:
 30 <221> NAME/KEY: 5'UTR
 31 <222> LOCATION: (1)..(38)
 33 <220> FEATURE:
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 35 <222> LOCATION: (39)..(2438)
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 39 <222> LOCATION: (2439)..(2506)
 41 <220> FEATURE:
 42 <221> NAME/KEY: polyA_site
 43 <222> LOCATION: (2507)..(2527)
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 48 1 5
 50 cat cgc gga gag aag gag gcg gcc ggg acg acg gcg ggc acc 104
 51 His Arg Gly Glu Lys Glu Ala Ala Gly Thr Thr Ala Ala Gly Thr
 52 10 15 20
 54 ggg ggt gcc acc gag cag ccg ccg cac ccg gaa cac aaa aaa cac 152
 55 Gly Gly Ala Thr Glu Gln Pro Pro Arg His Arg Glu His Lys Lys His
 56 25 30 35
 58 aag cac ccg agt ggc agt ggc ggt agc ggt ggc gaa cga ccg aag 200
 59 Lys His Arg Ser Gly Gly Ser Gly Gly Glu Arg Arg Lys
 60 40 45 50

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62 cgg agc cg_g gaa cgt ggg ggc gag cgc ggg agc ggg cgg cgc ggg gcc 248
 63 Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly Ser Gly Arg Arg Gly Ala
 64 55 60 65 70
 66 gaa gct gag gcc cgg agc agc acg cac ggg cgg gag cgc agc cag gca 296
 67 Glu Ala Glu Ala Arg Ser Ser Thr His Gly Arg Glu Arg Ser Gln Ala
 68 75 80 85
 70 gag ccc tcc gag cgg cgc gtg aag cgg gag aag cgc gat gac ggc tac 344
 71 Glu Pro Ser Glu Arg Arg Val Lys Arg Glu Lys Arg Asp Asp Gly Tyr
 72 90 95 100
 74 gag gcc gct gcc agc tcc aaa act agc tca ggc gat gcc tcc tca ctc 392
 75 Glu Ala Ala Ala Ser Ser Lys Thr Ser Ser Gly Asp Ala Ser Ser Leu
 76 105 110 115
 78 agc atc gag gag act aac aaa ctc cgg gca aag ttg ggg ctg aaa ccc 440
 79 Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala Lys Leu Gly Leu Lys Pro
 80 120 125 130
 82 ttg gag gtt aat gcc atc aag aag gag ggc acc aag gag gag ccc 488
 83 Leu Glu Val Asn Ala Ile Lys Lys Glu Ala Gly Thr Lys Glu Glu Pro
 84 135 140 145 150
 86 gtg aca gct gat gtc atc aac cct atg gcc ttg cga cag cga gag 536
 87 Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg Gln Arg Glu Glu
 88 155 160 165
 90 ctg cgg gag aag ctg gcg gct gcc aag gag aag cgc ctg ctg aac caa 584
 91 Leu Arg Glu Lys Leu Ala Ala Lys Glu Lys Arg Leu Leu Asn Gln
 92 170 175 180
 94 aag ctg ggg aag ata aag acc cta gga gag gat gac ccc tgg ctg gac 632
 95 Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp Pro Trp Leu Asp
 96 185 190 195
 98 gac act gca gcc tgg atc gag agg agc cgg cag ctg cag aag gag aag 680
 99 Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu Gln Lys Glu Lys
 100 200 205 210
 102 gac ctg gca gag aag agg gcc aag tta ctg gag gag atg gac caa gag 728
 103 Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu Met Asp Gln Glu
 104 215 220 225 230
 106 ttt ggt gtc agc act ctg gtg gag gag gat ttc ggg cag agg cgg cag 776
 107 Phe Gly Val Ser Thr Leu Val Glu Glu Phe Gly Gln Arg Arg Gln
 108 235 240 245
 110 gac ctg tac agt gcc cgg gac ctg cag ggc ctc acc gtg gag cat gcc 824
 111 Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr Val Glu His Ala
 112 250 255 260
 114 att gat tcc ttc cga gaa ggg gag aca atg att ctt acc ctc aag gac 872
 115 Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu Thr Leu Lys Asp
 116 265 270 275
 118 aaa ggc gtg ctg cag gag gag gac gtg ctg gtg aac gtg aac ctg 920
 119 Lys Gly Val Leu Gln Glu Glu Asp Val Leu Val Asn Val Asn Leu
 120 280 285 290
 122 gtg gat aag gag cgg gca gag aaa aat gtg gag ctg cgg aag aag aag 968
 123 Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu Arg Lys Lys Lys
 124 295 300 305 310
 126 cct gac tac ctg ccc tat gcc gag gac gag agc gtg gac gac ctg gcg 1016

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128				315				320							325		
130	cag	caa	aaa	cct	cgc	tct	atc	ctg	tcc	aag	tat	gac	gaa	gag	ctt	gaa	1064
131	Gln	Gln	Lys	Pro	Arg	Ser	Ile	Leu	Ser	Lys	Tyr	Asp	Glu	Glu	Leu	Glu	
132					330				335						340		
134	ggg	gag	cgg	cca	cat	tcc	ttc	cgc	ttg	gag	cag	ggc	ggc	acg	gct	gat	1112
135	Gly	Glu	Arg	Pro	His	Ser	Phe	Arg	Leu	Glu	Gln	Gly	Gly	Thr	Ala	Asp	
136				345				350							355		
138	ggc	ctg	cgg	gag	cgg	gag	ctg	gag	gag	atc	cgg	gcc	aag	ctg	cgg	ctg	1160
139	Gly	Leu	Arg	Glu	Arg	Glu	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Leu	Arg	Leu	
140				360				365							370		
142	cag	gct	cag	tcc	ctg	agc	aca	gtg	ggg	ccc	cgg	ctg	gcc	tcc	gaa	tac	1208
143	Gln	Ala	Gln	Ser	Leu	Ser	Thr	Val	Gly	Pro	Arg	Leu	Ala	Ser	Glu	Tyr	
144		375				380					385				390		
146	ctc	acg	cct	gag	gag	atg	gtg	acc	ttt	aaa	aag	acc	aag	cgg	agg	gtg	1256
147	Leu	Thr	Pro	Glu	Glu	Met	Val	Thr	Phe	Lys	Lys	Thr	Lys	Arg	Arg	Val	
148						395				400					405		
150	aag	aaa	atc	cgc	aag	aag	gag	aag	gag	gta	gta	gtg	cgg	gca	gat	gac	1304
151	Lys	Lys	Ile	Arg	Lys	Lys	Glu	Lys	Glu	Val	Val	Val	Arg	Ala	Asp	Asp	
152					410				415						420		
154	ttg	ctg	cct	ctc	ggg	gac	cag	act	cag	gat	ggg	gac	ttt	ggt	tcc	aga	1352
155	Leu	Leu	Pro	Leu	Gly	Asp	Gln	Thr	Gln	Asp	Gly	Asp	Phe	Gly	Ser	Arg	
156					425				430						435		
158	ctg	cgg	gga	cgg	ggt	cgc	cgc	cga	gtg	tcc	gaa	gtg	gag	gag	gag	aag	1400
159	Leu	Arg	Gly	Arg	Gly	Arg	Arg	Val	Ser	Glu	Val	Glu	Glu	Glu	Lys		
160					440				445						450		
162	gag	cct	gtg	cct	cag	ccc	ctg	ccg	tcg	gac	gac	acc	cga	gtg	gag	aac	1448
163	Glu	Pro	Val	Pro	Gln	Pro	Leu	Pro	Ser	Asp	Asp	Thr	Arg	Val	Glu	Asn	
164		455					460				465				470		
166	atg	gac	atc	agt	gat	gag	gag	gaa	ggt	gga	gct	cca	ccg	ccg	ggg	tcc	1496
167	Met	Asp	Ile	Ser	Asp	Glu	Glu	Gly	Gly	Ala	Pro	Pro	Pro	Gly	Ser		
168					475				480						485		
170	ccg	cag	gtg	ctg	gag	gag	gac	gag	gcg	gag	ctg	cag	aag	cag		1544	
171	Pro	Gln	Val	Leu	Glu	Glu	Asp	Glu	Ala	Glu	Leu	Glu	Leu	Gln	Lys	Gln	
172					490				495						500		
174	ctg	gag	aag	gga	cgc	cgg	ctg	cga	cag	tta	cag	cag	cta	cag	cag	ctg	1592
175	Leu	Glu	Lys	Gly	Arg	Arg	Leu	Arg	Gln	Leu	Gln	Gln	Leu	Gln	Gln	Leu	
176					505				510						515		
178	cga	gac	agt	ggc	gag	aag	gtg	gtg	gag	att	gtg	aag	aag	ctg	gag	tct	1640
179	Arg	Asp	Ser	Gly	Glu	Lys	Val	Val	Glu	Ile	Val	Lys	Lys	Leu	Glu	Ser	
180					520				525						530		
182	cgc	cag	cgg	ggc	tgg	gag	gag	gat	gag	gat	ccc	gag	cgg	aag	ggg	gcc	1688
183	Arg	Gln	Arg	Gly	Trp	Glu	Glu	Asp	Glu	Asp	Pro	Glu	Arg	Lys	Gly	Ala	
184		535					540				545				550		
186	atc	gtg	ttc	aac	gcc	acg	tcc	gag	ttc	tgc	cgc	acc	ttg	ggg	gag	atc	1736
187	Ile	Val	Phe	Asn	Ala	Thr	Ser	Glu	Phe	Cys	Arg	Thr	Leu	Gly	Glu	Ile	
188					555				560						565		
190	ccc	acc	tac	ggg	ctg	gct	ggc	aat	cgc	gag	gag	cag	gag	gag	ctc	atg	1784
191	Pro	Thr	Tyr	Gly	Leu	Ala	Gly	Asn	Arg	Glu	Glu	Gln	Glu	Glu	Leu	Met	

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192	570	575	580			
194	gac ttt gaa	cg ^g gat gag gag	cg ^c tca	gcc aac ggt ggc tcc gaa tct	1832	
195	Asp Phe	Glu Arg	Asp Glu	Glu Arg Ser Ala Asn Gly	Gly Ser Glu Ser	
196	585	590	595			
198	gac ggg gag gag	aac atc ggc tgg	agc acg gtg	aac ctg gac gag gag	1880	
199	Asp Gly	Glu Glu	Asn Ile	Gly Trp Ser Thr Val Asn	Leu Asp Glu Glu	
200	600	605	610			
202	aag cag cag cag	gat ttc tct	gct tcc acc acc	atc ctg gac gag	1928	
203	Lys Gln	Gln Gln	Asp Phe	Ser Ser Ala Ser Thr	Thr Ile Leu Asp Glu	
204	615	620	625	630		
206	gaa ccg atc gtg	aat agg ggg	ctg gca	gct gcc ctg ctc ctg tgt	cag 1976	
207	Glu Pro	Ile Val	Asn Arg	Gly Leu Ala Ala	Leu Leu Leu Cys Gln	
208	635	640	645			
210	aac aaa ggg	ctg ctg gag	acc aca	gtg cag aag	gtg gcc cg ^g gtg aag 2024	
211	Asn Lys	Gly Leu	Leu Glu	Thr Thr Val Gln	Lys Val Ala Arg Val Lys	
212	650	655	660			
214	gcc ccc aac aag	tcg ctg ccc	tca gcc	gtg tac tgc atc	gag gat aag 2072	
215	Ala Pro	Asn Lys	Ser Leu	Pro Ser Ala Val	Tyr Cys Ile Glu Asp Lys	
216	665	670	675			
218	atg gcc atc	gat gac aag	tac agc	cg ^g agg gag	gaa tac cga ggc ttc 2120	
219	Met Ala	Ile Asp	Asp Lys	Tyr Ser Arg Arg	Glu Glu Tyr Arg Gly Phe	
220	680	685	690			
222	aca cag gac	tac aag gag	aag gac	ggc tac aaa	ccc gac gtt aag atc 2168	
223	Thr Gln	Asp Phe	Lys Glu	Lys Asp Gly	Tyr Lys Pro Asp Val Lys Ile	
224	695	700	705	710		
226	gaa tac	gtg gat gag	acg ggc	cg ^g aaa	ctc aca ccc aag gag gct ttc 2216	
227	Glu Tyr	Val Asp	Glu Thr	Gly Arg Lys	Leu Thr Pro Lys Glu Ala Phe	
228	715	720	725			
230	cg ^g cag	ctg tcg	cac cg ^c	tcc cat	ggc aag ggc tca	ggc aag atg aag 2264
231	Arg Gln	Leu Ser	His Arg	Phe His	Gly Lys Gly Ser Gly	Lys Met Lys
232	730	735	740			
234	aca gag	cg ^g cg ^g	atg aag	aag ctg	gac gag gag	g ^c ctc ctg aag aag 2312
235	Thr Glu	Arg Arg	Met Lys	Lys Leu	Asp Glu Ala Leu	Leu Lys Lys
236	745	750	755			
238	atg agc	tcc agc	gac acg	ccc ctg	ggc acc gtg	gcc ctg ctc cag gag 2360
239	Met Ser	Ser Ser	Asp Thr	Pro Leu	Gly Thr Val	Ala Leu Leu Gln Glu
240	760	765	770			
242	aag cag	aag gct	cag aag	acc ccc	tac atc	gtg ctc agc ggc agc ggc 2408
243	Lys Gln	Lys Ala	Gln Lys	Thr Pro	Tyr Ile Val	Leu Ser Gly Ser Gly
244	775	780	785	790		
246	aag agc	atg aac	g ^c aac	acc atc	acc aag	tgacagcgcc ctccccgtagt 2458
247	Lys Ser	Met Asn	Ala Asn	Thr Ile	Thr Lys	
248	795	800				
250	cg ^g ccctgcc	tcaaccttca	tattaaataa	agctccctcc	ttat ^t tttaa	aaaaaaaaaaaa 2518
252	aaaaaaaaaa					2527
255	<210>	SEQ ID NO:	2			
256	<211>	LENGTH:	800			
257	<212>	TYPE:	PRT			
258	<213>	ORGANISM:	Homo sapiens			

RAW SEQUENCE LISTING
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 262 1 5 10 15
 264 Thr Ala Ala Ala Gly Thr Gly Gly Ala Thr Glu Gln Pro Pro Arg His
 265 20 25 30
 267 Arg Glu His Lys Lys His Lys His Arg Ser Gly Gly Ser Gly Ser
 268 35 40 45
 270 Gly Gly Glu Arg Arg Lys Arg Ser Arg Glu Arg Gly Gly Glu Arg Gly
 271 50 55 60
 273 Ser Gly Arg Arg Gly Ala Glu Ala Glu Ala Arg Ser Ser Thr His Gly
 274 65 70 75 80
 276 Arg Glu Arg Ser Gln Ala Glu Pro Ser Glu Arg Arg Val Lys Arg Glu
 277 85 90 95
 279 Lys Arg Asp Asp Gly Tyr Glu Ala Ala Ser Ser Lys Thr Ser Ser
 280 100 105 110
 282 Gly Asp Ala Ser Ser Leu Ser Ile Glu Glu Thr Asn Lys Leu Arg Ala
 283 115 120 125
 285 Lys Leu Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala
 286 130 135 140
 288 Gly Thr Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala
 289 145 150 155 160
 291 Leu Arg Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu
 292 165 170 175
 294 Lys Arg Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu
 295 180 185 190
 297 Asp Asp Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg
 298 195 200 205
 300 Gln Leu Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu
 301 210 215 220
 303 Glu Glu Met Asp Gln Glu Phe Gly Val Ser Thr Leu Val Glu Glu
 304 225 230 235 240
 306 Phe Gly Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly
 307 245 250 255
 309 Leu Thr Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met
 310 260 265 270
 312 Ile Leu Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Asp Val
 313 275 280 285
 315 Leu Val Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val
 316 290 295 300
 318 Glu Leu Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu
 319 305 310 315 320
 321 Ser Val Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys
 322 325 330 335
 324 Tyr Asp Glu Glu Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu
 325 340 345 350
 327 Gln Gly Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile
 328 355 360 365
 330 Arg Ala Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro
 331 370 375 380

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/202,047A

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